

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/593,842

Source: IFWP

Date Processed by STIC: 10/3/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 10/03/2006

PATENT APPLICATION: US/10/593,842

TIME: 09:00:37

Input Set : A:\082368-000510US.txt

Output Set: N:\CRF4\10032006\J593842.raw

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3 <110> APPLICANT: Nakamura, Yusuke
4     Daigo, Yataro
5     Nakatsuru, Shuichi
7 <120> TITLE OF INVENTION: METHOD FOR DIAGNOSING NON-SMALL CELL
8     LUNG CANCER
10 <130> FILE REFERENCE: 082368-000510US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/593,842
C--> 12 <141> CURRENT FILING DATE: 2006-09-22
12 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/005613
13 <151> PRIOR FILING DATE: 2005-03-18
15 <150> PRIOR APPLICATION NUMBER: US 60/555,789
16 <151> PRIOR FILING DATE: 2004-03-23
18 <160> NUMBER OF SEQ ID NOS: 127
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 4908
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (141)..(3311)
32 <400> SEQUENCE: 1
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35 cccctgtcgg cgccaagccc ctccgcccct cacagcgccc aggtccgcgg cggggccttg      120
37 attttttggc ggggaccgtc atg gcg tgc cag cca aat tgc tct gcg aag aag      173
38             Met Ala Ser Gln Pro Asn Ser Ser Ala Lys Lys
39             1             5             10
41 aaa gag gag aag ggg aag aac atc cag gtg gtg gtg aga tgc aga cca      221
42 Lys Glu Glu Lys Gly Lys Asn Ile Gln Val Val Val Arg Cys Arg Pro
43             15             20             25
45 ttt aat ttg gca gag cgg aaa gct agc gcc cat tca ata gta gaa tgt      269
46 Phe Asn Leu Ala Glu Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys
47             30             35             40
49 gat cct gta cga aaa gaa gtt agt gta cga act gga gga ttg gct gac      317
50 Asp Pro Val Arg Lys Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp
51             45             50             55
53 aag agc tca agg aaa aca tac act ttt gat atg gtg ttt gga gca tct      365
54 Lys Ser Ser Arg Lys Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser
55 60             65             70             75
57 act aaa cag att gat gtt tac cga agt gtt gtt tgt cca att ctg gat      413
58 Thr Lys Gln Ile Asp Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp
59             80             85             90
61 gaa gtt att atg ggc tat aat tgc act atc ttt gcg tat ggc caa act      461

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66	Gly	Thr	Gly	Lys	Thr	Phe	Thr	Met	Glu	Gly	Glu	Arg	Ser	Pro	Asn	Glu	
67			110					115					120				
69	gag	tat	acc	tgg	gaa	gag	gat	ccc	ttg	gct	ggt	ata	att	cca	cgt	acc	557
70	Glu	Tyr	Thr	Trp	Glu	Glu	Asp	Pro	Leu	Ala	Gly	Ile	Ile	Pro	Arg	Thr	
71		125					130					135					
73	ctt	cat	caa	att	ttt	gag	aaa	ctt	act	gat	aat	ggt	act	gaa	ttt	tca	605
74	Leu	His	Gln	Ile	Phe	Glu	Lys	Leu	Thr	Asp	Asn	Gly	Thr	Glu	Phe	Ser	
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77	gtc	aaa	gtg	tct	ctg	ttg	gag	atc	tat	aat	gaa	gag	ctt	ttt	gat	ctt	653
78	Val	Lys	Val	Ser	Leu	Leu	Glu	Ile	Tyr	Asn	Glu	Glu	Leu	Phe	Asp	Leu	
79				160					165					170			
81	ctt	aat	cca	tca	tct	gat	gtt	tct	gag	aga	cta	cag	atg	ttt	gat	gat	701
82	Leu	Asn	Pro	Ser	Ser	Asp	Val	Ser	Glu	Arg	Leu	Gln	Met	Phe	Asp	Asp	
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94	Lys	Arg	Thr	Thr	Ala	Ala	Thr	Leu	Met	Asn	Ala	Tyr	Ser	Ser	Arg	Ser	
95	220				225				230					235			
97	cac	tca	gtt	ttc	tct	gtt	aca	ata	cat	atg	aaa	gaa	act	acg	att	gat	893
98	His	Ser	Val	Phe	Ser	Val	Thr	Ile	His	Met	Lys	Glu	Thr	Thr	Ile	Asp	
99			240					245				250					
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102	Gly	Glu	Glu	Leu	Val	Lys	Ile	Gly	Lys	Leu	Asn	Leu	Val	Asp	Leu	Ala	
103			255					260				265					
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106	Gly	Ser	Glu	Asn	Ile	Gly	Arg	Ser	Gly	Ala	Val	Asp	Lys	Arg	Ala	Arg	
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114	Thr	Ala	Leu	Val	Glu	Arg	Thr	Pro	His	Val	Pro	Tyr	Arg	Glu	Ser	Lys	
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117	cta	act	aga	atc	ctc	cag	gat	tct	ctt	gga	ggg	cgt	aca	aga	aca	tct	1133
118	Leu	Thr	Arg	Ile	Leu	Gln	Asp	Ser	Leu	Gly	Gly	Arg	Thr	Arg	Thr	Ser	
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121	ata	att	gca	aca	att	tct	cct	gca	tct	ctc	aat	ctt	gag	gaa	act	ctg	1181
122	Ile	Ile	Ala	Thr	Ile	Ser	Pro	Ala	Ser	Leu	Asn	Leu	Glu	Glu	Thr	Leu	
123			335					340				345					
125	agt	aca	ttg	gaa	tat	gct	cat	aga	gca	aag	aac	ata	ttg	aat	aag	cct	1229
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133	gag gag ata gaa cgt tta aaa cga gat ctt gct gca gcc cgt gag aaa	1325		
134	Glu Glu Ile Glu Arg Leu Lys Arg Asp Leu Ala Ala Arg Glu Lys			
135	380 385 390 395			
137	aat gga gtg tat att tct gaa gaa aat ttt aga gtc atg agt gga aaa	1373		
138	Asn Gly Val Tyr Ile Ser Glu Glu Asn Phe Arg Val Met Ser Gly Lys			
139	400 405 410			
141	tta act gtt caa gaa gag cag att gta gaa ttg att gaa aaa att ggt	1421		
142	Leu Thr Val Gln Glu Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly			
143	415 420 425			
145	gct gtt gag gag gag ctg aat agg gtt aca gag ttg ttt atg gat aat	1469		
146	Ala Val Glu Glu Glu Leu Asn Arg Val Thr Glu Leu Phe Met Asp Asn			
147	430 435 440			
149	aaa aat gaa ctt gac cag tgt aaa tct gac ctg caa aat aaa aca caa	1517		
150	Lys Asn Glu Leu Asp Gln Cys Lys Ser Asp Leu Gln Asn Lys Thr Gln			
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153	gaa ctt gaa acc act caa aaa cat ttg caa gaa act aaa tta caa ctt	1565		
154	Glu Leu Glu Thr Thr Gln Lys His Leu Gln Glu Thr Lys Leu Gln Leu			
155	460 465 470 475			
157	gtt aaa gaa gaa tat atc aca tca gct ttg gaa agt act gag gag aaa	1613		
158	Val Lys Glu Glu Tyr Ile Thr Ser Ala Leu Glu Ser Thr Glu Glu Lys			
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161	ctt cat gat gct gcc agc aag ctg ctt aac aca gtt gaa gaa act aca	1661		
162	Leu His Asp Ala Ala Ser Lys Leu Leu Asn Thr Val Glu Glu Thr Thr			
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165	aaa gat gta tct ggt ctc cat tcc aaa ctg gat cgt aag aag gca gtt	1709		
166	Lys Asp Val Ser Gly Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val			
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169	gac caa cac aat gca gaa gct cag gat att ttt ggc aaa aac ctg aat	1757		
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173	agt ctg ttt aat aat atg gaa gaa tta att aag gat ggc agc tca aag	1805		
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177	caa aag gcc atg cta gaa gta cat aag acc tta ttt ggt aat ctg ctg	1853		
178	Gln Lys Ala Met Leu Glu Val His Lys Thr Leu Phe Gly Asn Leu Leu			
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181	tct tcc agt gtc tct gca tta gat acc att act aca gta gca ctt gga	1901		
182	Ser Ser Ser Val Ser Ala Leu Asp Thr Ile Thr Thr Val Ala Leu Gly			
183	575 580 585			
185	tct ctc aca tct att cca gaa aat gtg tct act cat gtt tct cag att	1949		
186	Ser Leu Thr Ser Ile Pro Glu Asn Val Ser Thr His Val Ser Gln Ile			
187	590 595 600			
189	ttt aat atg ata cta aaa gaa caa tca tta gca gca gaa agt aaa act	1997		
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198	Leu	Glu	Met	Ile	Leu	Ser	Pro	Thr	Val	Val	Ser	Ile	Leu	Lys	Ile	Asn	
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205	ata	gaa	gat	caa	aaa	aag	gaa	cta	gat	ggc	ttt	ctc	agt	ata	ctg	tgt	2189
206	Ile	Glu	Asp	Gln	Lys	Lys	Glu	Leu	Asp	Gly	Phe	Leu	Ser	Ile	Leu	Cys	
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209	aac	aat	cta	cat	gaa	cta	caa	gaa	aat	acc	att	tgt	tcc	ttg	gtt	gag	2237
210	Asn	Asn	Leu	His	Glu	Leu	Gln	Glu	Asn	Thr	Ile	Cys	Ser	Leu	Val	Glu	
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213	tca	caa	aag	caa	tgt	gga	aac	cta	act	gaa	gac	ctg	aag	aca	ata	aag	2285
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225	agt	agt	gtc	cag	gaa	aat	ata	cag	cag	aaa	tct	aag	gat	ata	gtc	aac	2429
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241	tct	caa	gag	act	gaa	cag	aga	tgt	gaa	tct	ctg	aac	aca	aga	aca	gtt	2621
242	Ser	Gln	Glu	Thr	Glu	Gln	Arg	Cys	Glu	Ser	Leu	Asn	Thr	Arg	Thr	Val	
243					815						820					825	
245	tat	ttt	tct	gaa	cag	tgg	gta	tct	tcc	tta	aat	gaa	agg	gaa	cag	gaa	2669
246	Tyr	Phe	Ser	Glu	Gln	Trp	Val	Ser	Ser	Leu	Asn	Glu	Arg	Glu	Gln	Glu	
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253	tca	gac	atc	act	gag	aaa	tca	gat	gga	cgt	aag	gca	gct	cat	gag	aaa	2765
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262 Ile Ala Gln Asn Leu Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr
263          895          900          905
265 aag ctt aat tgc ttt ctg gaa cag gat ctg aaa ctg gat atc cca aca      2909
266 Lys Leu Asn Cys Phe Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr
267          910          915          920
269 ggt acg aca cca cag agg aaa agt tat tta tac cca tca aca ctg gta      2957
270 Gly Thr Thr Pro Gln Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val
271          925          930          935
273 aga act gaa cca cgt gaa cat ctc ctt gat cag ctg aaa agg aaa cag      3005
274 Arg Thr Glu Pro Arg Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln
275 940          945          950          955
277 cct gag ctg tta atg atg cta aac tgt tca gaa aac aac aaa gaa gag      3053
278 Pro Glu Leu Leu Met Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu
279          960          965          970
281 aca att ccg gat gtg gat gta gaa gag gca gtt ctg ggg cag tat act      3101
282 Thr Ile Pro Asp Val Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr
283          975          980          985
285 gaa gaa cct cta agt caa gag cca tct gta gat gct ggt gtg gat tgt      3149
286 Glu Glu Pro Leu Ser Gln Glu Pro Ser Val Asp Ala Gly Val Asp Cys
287          990          995          1000
289 tca tca att ggc ggg gtt cca ttt ttc cag cat aaa aaa tca cat      3194
290 Ser Ser Ile Gly Gly Val Pro Phe Phe Gln His Lys Lys Ser His
291          1005          1010          1015
293 gga aaa gac aaa gaa aac aga ggc att aac aca ctg gag agg tct      3239
294 Gly Lys Asp Lys Glu Asn Arg Gly Ile Asn Thr Leu Glu Arg Ser
295          1020          1025          1030
297 aaa gtg gaa gaa act aca gag cac ttg gtt aca aag agc aga tta      3284
298 Lys Val Glu Glu Thr Thr Glu His Leu Val Thr Lys Ser Arg Leu
299          1035          1040          1045
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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Seq#:127

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date